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R. Hulsey
 RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/254,344

DATE: 04/30/2001
 TIME: 13:26:48

Input Set : A:\024705-077.ST25.txt
 Output Set: N:\CRF3\04302001\I254344.raw

P.S
ENTERED

4 <110> APPLICANT: HAYASHIZAKI, Yoshihide
 5 WATAHIKI, Masanori
 7 <120> TITLE OF INVENTION: RNA Polymerase
 9 <130> FILE REFERENCE: 024705-077
 11 <140> CURRENT APPLICATION NUMBER: US 09/254,344
 12 <141> CURRENT FILING DATE: 1999-09-03
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03037
 15 <151> PRIOR FILING DATE: 1998-07-06
 17 <150> PRIOR APPLICATION NUMBER: JP 9/180883
 18 <151> PRIOR FILING DATE: 1997-07-07
 20 <150> PRIOR APPLICATION NUMBER: JP 10/155759
 21 <151> PRIOR FILING DATE: 1998-06-04
 23 <160> NUMBER OF SEQ ID NOS: 23
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2659
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Bacteriophage T7
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (10)..(2658)
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 39 1 5 10
 41 gaa ctg gct gtc atc ccg ttc aac act ctg gct gac cat tac ggt gag 99
 42 Glu Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu
 43 15 20 25 30
 45 cgt tta gct cgc gaa cag ttg gcc ctt gag cat gag tct tac gag atg 147
 46 Arg Leu Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met
 47 35 40 45
 49 ggt gaa gca cgc ttc cgc aag atg ttt gag cgt caa ctt aaa gct ggt 195
 50 Gly Glu Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly
 51 50 55 60
 53 gag gtt gcg gat aac gct gcc gcc aag cct ctc atc act acc cta ctc 243
 54 Glu Val Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu
 55 65 70 75
 57 cct aag atg att gca cgc atc aac gac tgg ttt gag gaa gtg aaa gct 291
 58 Pro Lys Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala
 59 80 85 90
 61 aag cgc ggc aag cgc ccg aca gcc ttc cag ttc ctg caa gaa atc aag 339
 62 Lys Arg Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys
 63 95 100 105 110
 65 ccg gaa gcc gta cgc tac atc acc att aag acc act ctg gct tgc cta 387
 66 Pro Glu Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu
 67 115 120 125
 69 acc agt gct gac aat aca acc gtt cag gct gta gca agc gca atc ggt 435

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71									130						140	
73	cgg	gcc	att	gag	gac	gag	gct	cgc	ttc	ggg	cgt	atc	cgt	gac	ctt	gaa
74	Arg	Ala	Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu
75									145						155	
77	gct	aag	cac	ttc	aag	aaa	aac	gtt	gag	gaa	caa	ctc	aac	aag	cgc	gta
78	Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val
79									160						170	
81	ggg	cac	gtc	tac	aag	aaa	gca	ttt	atg	caa	gtt	gtc	gag	gct	gac	atg
82	Gly	His	Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met
83	175								180						185	
85	ctc	tct	aag	ggt	cta	ctc	ggt	ggc	gag	gcg	tgg	tct	tgc	tgg	cat	aag
86	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys
87									195						200	
89	gaa	gac	tct	att	cat	gta	gga	gta	cgc	tgc	atc	gag	atg	ctc	att	gag
90	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu	Met	Leu	Ile	Glu
91									210						215	
93	tca	acc	gga	atg	gtt	agc	tta	cac	cgc	caa	aat	gct	ggc	gta	gta	ggt
94	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	Ala	Gly	Val	Val	Gly
95									225						230	
97	caa	gac	tct	gag	act	atc	gaa	ctc	gca	cct	gaa	taa	gct	gag	gct	atc
98	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	Tyr	Ala	Glu	Ala	Ile
99									240						245	
101	gca	acc	cgt	gca	ggt	gct	ctg	gct	ggc	atc	tct	ccg	atg	ttc	caa	cct
102	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	Phe	Gln	Pro
103	255								260						265	
105	tgc	gta	gtt	cct	cct	aag	ccg	tgg	act	ggc	att	act	ggt	ggt	ggc	tat
106	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	Thr	Gly	Gly	Tyr	
107									275						280	
109	tgg	gct	aac	ggt	cgt	cgt	cct	ctg	gct	ctg	gtg	cgt	act	cac	agt	aag
110	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys
111									290						295	
113	aaa	gca	ctg	atg	cgc	tac	gaa	gac	gtt	tac	atg	cct	gag	gtg	tac	aaa
114	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	Tyr	Lys
115									305						310	
117	gcg	att	aac	att	gcg	caa	aac	acc	gca	tgg	aaa	atc	aac	aag	aaa	gtc
118	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	Lys	Val
119									320						325	
121	cta	gcg	gtc	gcc	aac	gta	atc	acc	aag	tgg	aag	cat	tgt	ccg	gtc	gag
122	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	His	Cys	Pro	Val	Glu
123	335								340						345	
125	gac	atc	cct	gct	att	gag	cgt	gaa	gaa	ctc	ccg	atg	aaa	ccg	gaa	gac
126	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	Met	Lys	Pro	Glu	Asp
127									355						360	
129	atc	gac	atg	aat	cct	gag	gct	ctc	acc	gct	tgg	aaa	cgt	gct	gcc	gct
130	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp	Lys	Arg	Ala	Ala	Ala
131									370						375	
133	gct	gtg	tac	cgc	aag	gac	aag	gct	cgc	aag	tct	ccg	cgt	atc	agc	ctt
134	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser	Arg	Arg	Ile	Ser	Leu
135									380						385	

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135	385	390	395	
137	gag ttc atg ctt gag caa gcc aat aag ttt gct aac cat aag gcc atc			1251
138	Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile			
139	400	405	410	
141	tgg ttc cct tac aac atg gac tgg cgc ggt cgt gtt tac gct gtg tca			1299
142	Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser			
143	415	420	425	430
145	atg ttc aac ccg caa ggt aac gat atg acc aaa gga ctg ctt acg ctg			1347
146	Met Phe Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu			
147	435	440	445	
149	gcg aaa ggt aaa cca atc ggt aag gaa ggt tac tac tgg ctg aaa atc			1395
150	Ala Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile			
151	450	455	460	
153	cac ggt gca aac tgt gcg ggt gtc gat aag gtt ccg ttc cct gag cgc			1443
154	His Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg			
155	465	470	475	
157	atc aag ttc att gag gaa aac cac gag aac atc atg gct tgc gct aag			1491
158	Ile Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys			
159	480	485	490	
161	tct cca ctg gag aac act tgg tgg gct gag caa gat tct ccg ttc tgc			1539
162	Ser Pro Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys			
163	495	500	505	510
165	ttc ctt gcg ttc tgc ttt gag tac gct ggg gta cag cac cac ggc ctg			1587
166	Phe Leu Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu			
167	515	520	525	
169	agc tat aac tgc tcc ctt ccg ctg gcg ttt gac ggg tct tgc tct ggc			1635
170	Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly			
171	530	535	540	
173	atc cag cac ttc tcc gcg atg ctc cga gat gag gta ggt ggt cgc gcg			1683
174	Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala			
175	545	550	555	
177	gtt aac ttg ctt cct agt gaa acc gtt cag gac atc tac ggg att gtt			1731
178	Val Asn Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val			
179	560	565	570	
181	gct aag aaa gtc aac gag att cta caa gca gac gca atc aat ggg acc			1779
182	Ala Lys Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr			
183	575	580	585	590
185	gat aac gaa gta gtt acc gtg acc gat gag aac act ggt gaa atc tct			1827
186	Asp Asn Glu Val Val Thr Val Asp Glu Asn Thr Gly Glu Ile Ser			
187	595	600	605	
189	gag aaa gtc aag ctg ggc act aag gca ctg gct ggt caa tgg ctg gct			1875
190	Glu Lys Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala			
191	610	615	620	
193	tac ggt gtt act cgc agt gtg act aag cgt tca gtc atg acg ctg gct			1923
194	Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala			
195	625	630	635	
197	tac ggg tcc aaa gag ttc ggc ttc cgt caa caa gtg ctg gaa gat acc			1971
198	Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr			
199	640	645	650	

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201 att cag cca gct att gat tcc ggc aag ggt ctg atg ttc act cag ccg	2019
202 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro	
203 655 660 665 670	
205 aat cag gct gct gga tac atg gct aag ctg att tgg gaa tct gtg agc	2067
206 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser	
207 675 680 685	
209 gtg acg gtg gta gct gcg gtt gaa gca atg aac tgg ctt aag tct gct	2115
210 Val Thr Val Val Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala	
211 690 695 700	
213 gct aag ctg ctg gct gct gag gtc aaa gat aag aag act gga gag att	2163
214 Ala Lys Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile	
215 705 710 715	
217 ctt cgc aag cgt tgc gct gtg cat tgg gta act cct gat ggt ttc cct	2211
218 Leu Arg Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro	
219 720 725 730	
221 gtg tgg cag gaa tac aag aag cct att cag acg cgc ttg aac ctg atg	2259
222 Val Trp Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met	
223 735 740 745 750	
225 ttc ctc ggt cag ttc cgc tta cag cct acc att aac acc aac aaa gat	2307
226 Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp	
227 755 760 765	
229 agc gag att gat gca cac aaa cag gag tct ggt atc gct cct aac ttt	2355
230 Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe	
231 770 775 780	
233 gta cac agc caa gac ggt agc cac ctt cgt aag act gta gtg tgg gca	2403
234 Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala	
235 785 790 795	
237 cac gag aag tac gga atc gaa tct ttt gca ctg att cac gac tcc ttc	2451
238 His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe	
239 800 805 810	
241 ggt acc att ccg gct gac gct gcg aac ctg ttc aaa gca gtg cgc gaa	2499
242 Gly Thr Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu	
243 815 820 825 830	
245 act atg gtt gac aca tat gag tct tgt gat gta ctg gct gat ttc tac	2547
246 Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr	
247 835 840 845	
249 gac cag ttc gct gac cag ttg cac gag tct caa ttg gac aaa atg cca	2595
250 Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro	
251 850 855 860	
253 gca ctt ccg gct aaa ggt aac ttg aac ctc cgt gac atc tta gag tcg	2643
254 Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser	
255 865 870 875	
257 gac ttc gcg ttc gcg t	2659
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259 880	
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263 <211> LENGTH: 883	
264 <212> TYPE: PRT	
265 <213> ORGANISM: Bacteriophage T7	

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267 <400> SEQUENCE: 2
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 272 Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
 273 20 25 30
 276 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 277 35 40 45
 280 Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 281 50 55 60
 284 Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 285 65 70 75 80
 288 Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 289 85 90 95
 292 Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 293 100 105 110
 296 Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 297 115 120 125
 300 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 301 130 135 140
 304 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 305 145 150 155 160
 308 His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 309 165 170 175
 312 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 313 180 185 190
 316 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 317 195 200 205
 320 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 321 210 215 220
 324 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 325 225 230 235 240
 328 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 329 245 250 255
 332 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 333 260 265 270
 336 Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 337 275 280 285
 340 Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 341 290 295 300
 344 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 345 305 310 315 320
 348 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 349 325 330 335
 352 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 353 340 345 350
 356 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 357 355 360 365
 360 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 361 370 375 380

Please Note:

Use f n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n r Xaa.

VERIFICATION SUMMARY

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L:1428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1516 M:283 W: Missing Blank Line separator, <220> field identifier
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23